Application of Robert Getts
Serial No. 09/802,162 filed 3/8/2001
Response of 9/24/2003 to Office Action of 3/24/2003

Remarks

Receipt is acknowledged of the Office Action of March 24, 2003 in the above-captioned matter. Reconsideration of the application and a three month extension of the time provided for a response are requested. The Commissioner is hereby authorized to charge Deposit Account 50-1604 for all amounts required.

In the Office Action, the claims of the application were provisionally rejected as being unpatentable over claims in co-pending applications 09/908,950 and 10/050,088, under the judicially created doctrine of obviousness-type double patenting. Applicant notes that the rejection is provisional, in view of the fact that the other claims have not been patented. Accordingly, it is respectfully requested that opportunity be provided to first ascertain what may be the scope of any approved claims in those co-pending applications before further action is required by Applicant or by the Patent Office. In the event that the rejection is maintained, it is believed that the rejection can be obviated, for example, via a terminal disclaimer.

In the Office Action, the claims were further rejected under 35 U.S.C. §103(a) based on Schena et al. (Science, Vol. 270, pp. 467-470, 1995) in view of Nilsen et al. (U.S. Patent No. 5,487,973). Further thereto, the claims have been amended to define the term "capture sequence", which term was previously set forth in all of the prior versions of the independent claims. Reconsideration of the rejections is respectfully requested.

As recited in the claims, the present invention uses a first component of cDNA reagents (the term comprising, having, and including being open terms, and being used interchangeably in the

claims). The cDNA reagents include a population of cDNAs reagents wherein there is a plurality of different cDNAs (i.e. cDNAs with different nucleotide sequences), but wherein those different cDNAs nonetheless have a common capture sequence. The capture sequence is used for hybridization of those various cDNAs to a complementary sequence provided as part of a capture reagent. In the preferred embodiment recited in the claims, the capture reagent is a dendrimer.

Accordingly, the present invention provides a method of high efficiency when a sample is provided for analysis, and that sample includes a plurality of different cDNAs. For example, in one application of the invention, cDNAs can be used that are reverse transcribed from a large population of mRNAs. Further to the invention, the capture reagent can hybridize to the capture sequence of any of those multiple cDNAs; thus, a single common sequence can be used to universally allow one type of capture reagent to hybridize to the many different cDNAs in the sample. This aspect of the invention is recited in Claims 1 and 18.

This method of the invention is highly advantageous as it avoids the need to create capture reagents for each of the different cDNAs – and is particularly useful since there are often an extremely large number of cDNAs in a sample. Neither Schena nor Nilsen nor their combination teach or suggest this method of the amended claims.

In Schena, for example, there is no teaching or suggestion of the use of a common capture sequence to hybridize a single type of capture reagent to any of multiple types of cDNAs obtained from a sample of mRNA. Schena does not appear to utilize such a method. Rather, Schena appears to label molecules using flourescein and lisamine labeled nucleotide analogs. *See e.g.*, Schena, p. 468, rightmost

column, first paragraph.

Likewise, the method disclosed in the Nilsen reference also does not teach or suggest a use of a capture sequence which is common to different cDNAs. In Nilsen, the dendrimer probes are created for analysis of the particular target nucleic acid which is to be studied. This is accomplished by synthesizing an arm for the dendrimer probe which will have a sequence complementary to a particular sequence on the target nucleic acid of interest. *See e.g.*, Col. 17 lines 30-54 and Col. 19 lines 45-60. The dendrimer that is created is specific to a particular target nucleic acid. Thus, Nilsen also does not teach a method using a common capture sequence for multiple cDNAs.

As discussed in the response to the prior Office Action, based on the disclosure of the Nilsen reference, a dendrimer probe would have to be synthesized for each of the cDNA sequences to be studied, if Nilsen were combined with another reference. When dealing with a microarray assay, for example, this would require the creation of thousands of different dendrimers, one for each cDNA copy of the different mRNA messages. This method would be extremely burdensome and impractical. The present invention, however, avoids this problem entirely. As a result, the present claims would not be obvious over the combination of the cited references.

Moreover, in further embodiments of the invention, reverse transcription is used to efficiently attach a common capture sequence onto multiple different types of cDNA sequences. This is recited, for example, in Claims 2 and 22. It allows a large population of mRNA sequences to be easily convertable into species easily hybridized to a capture reagent, without the need to create a separate capture reagent for each mRNA. This use of reverse transcription for attachment of a common capture

sequence is also not taught or suggested in the cited references.

In further embodiments of the invention, excess unhybridized RT primer is removed from the first component, as recited, for example, in Claims 3-4, 16-17 and 23-26. Limiting the amount of primer significantly improves the results obtained using the invention, and is also not taught or suggested in the cited references.

In view of the above, reconsideration of the application with favorable action on all of the pending claims is respectfully requested and believed fully warranted.

Dated: September 24, 2003

Respectfully submitted,

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